

## **REMARKS**

Claims 1-9 are pending in the instant application. With this Amendment, Claims 1, 2, 4 and 5-9 are canceled without prejudice, new Claims 10-14 are added and Claim 3 is amended. Thus, after entry of the present Amendment, Claims 3 and 10-14 are pending in the present application. For the PTO's convenience, a clean copy of pending Claims 3 and 10-14 are attached hereto as Exhibit B.

### **I. THE AMENDMENTS TO THE SPECIFICATION**

Pursuant to 37 CFR § 1.121(b)(3), Applicants file herewith a substitute specification. The substitute specification is substantially identical to the specification as originally filed. The margins of the specification have been altered to conform with the requirements of 37 CFR § 1.52. The substitute specification is otherwise identical to the specification as originally filed. As the substitute contains no new matter, entry thereof is respectfully requested.

Applicants have also amended the title of the specification to conform with the invention to which the elected claims are directed. As the amended title contains no new matter, entry thereof is respectfully requested.

### **II. THE AMENDMENT TO THE CLAIMS**

Applicants have canceled Claims 1, 2, 4 and 5-9 without prejudice, and Applicants have amended Claim 3 to correct minor errors in claim language and to conform with the election of SEQ ID NOS:9-18 for prosecution on their merits.

Applicants have added new Claims 10-14. New Claims 10-14 are fully supported by the specification and claims as originally filed. For instance, new Claims 10-11 are supported in the specification, for example, at page 16, lines 8-11, and by original Claim 1. New Claims 12-13 are supported in the specification, for example, at page 4, lines 10-12, and by original Claim 1. New Claim 14 is supported in the specification, for example, at page 16, line 27, through page 17, line 5, and at page 13, line 1, through page 14, line 3.

As the amendments are fully supported by the specification and claims as originally filed, they do not constitute new matter. Entry thereof is respectfully requested.

### **III. THE OBJECTION TO THE TITLE**

The title stands objected to because it is allegedly not descriptive of the present invention. Applicants submit that the amended title is descriptive of the invention to which the instant claims are directed and respectfully request that the objection to the title be withdrawn.

### **IV. THE OBJECTION TO THE SPECIFICATION**

The specification stands objected to because the margins are allegedly too small. Applicants submit that the margins of the substitute specification filed herewith meet the requirements of 37 CFR § 1.52 and respectfully request that the objection to the specification be withdrawn.

### **V. THE REJECTION UNDER 35 U.S.C. § 101 (UTILITY)**

Claims 1-4 stand rejected under 35 U.S.C. § 101 as allegedly lacking patentable utility. Applicants note that Claims 1, 2 and 4 have been canceled without prejudice with the present Amendment. Applicants respectfully traverse the rejection on the ground that Claim 3 is patentably useful.

According to 35 U.S.C. § 101, whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter may obtain a patent therefor subject to the conditions and requirements of 35 U.S.C. The threshold of utility is not high. *Juicy Whip Inc. v. Orange Bang Inc.*, 51 USPQ2d 1700, 1702 (Fed. Cir. 1999). An invention is “useful” under 35 U.S.C. § 101 if it is capable of providing some identifiable benefit. *Id.* (citing *Brenner v. Manson*, 383 U.S. 519, 534, 148 USPQ 689, 695 (1966)).

Claim 3 and new Claims 10-14 recite isolated polynucleotides corresponding to SEQ ID NOS:9-18. Such polynucleotides have tremendous identifiable benefits.

For instance, the claimed polynucleotides can be used to expand the utility of current genomic data such as human genomic data. Persons of skill in the art readily recognize the utility, both scientific and commercial, of genomic data from species such as humans and mice. For example, billions of dollars have been invested in the human genome project resulting in useful human genomic data. *See, e.g., Venter et al.*, 2001, *Science* 291:1304. The results have been a stunning success as the utility of human genomic data has been

widely recognized as a great gift to humanity. *See, e.g.,* Jasny and Kennedy, 2001, Science 291:1153. Technology that enhances the utility of useful genomic data is itself useful.

Current genomic data lacks necessary information that would make the data even more useful. For instance, of the myriad putative genes identified by the Human Genome Project, only a relatively small number are known to be expressed. Current technology struggles to separate expressed genes from “junk” DNA in the putative genes identified by massive sequencing efforts.

As disclosed in the specification at pages 1-2, isolated expressed DNA sequences from the human genome have tremendous utility in identifying the expressed genes in raw genomic sequences. Furthermore, the gene trapped sequences of the present invention overcome some of the limitations of conventional cDNA and expressed sequence tag libraries. In particular, the gene trapped sequences of the present invention, including SEQ ID NOS:9-18, were identified using reverse orientation retroviral gene trap vectors that nonspecifically integrate into the target cell genome. These gene trap vectors do not rely solely on the degree of endogenous mRNA expression of a gene for identification of that gene. Hence, the gene trap vectors are able to trap even poorly expressed genes. The identification of gene trapped sequences such as SEQ ID NOS:9-18 thus increases the value and utility of raw genomic data by enabling the identification of expressed genes, even poorly expressed genes, within the genomic data.

Furthermore, the specification provides numerous other credible, specific and substantial utilities for polynucleotides comprising SEQ ID NOS:9-18. For example, polynucleotides comprising SEQ ID NOS:9-18 can be used for diagnostic gene expression and analysis, for cross species hybridization analysis, antisense inhibition, gene targeting, identifying exon splice junctions, gene therapy, gene delivery and chromosome mapping. Each of these utilities is credible, specific and substantial.

For instance, at page 8, lines 14-21, the specification describes the utility of polynucleotides comprising SEQ ID NOS:9-18 for physical and genetic mapping of the human genome and/or the genome of model organisms. To illustrate, early gene mapping techniques relied on methods such as Giemsa staining to identify regions of chromosomes. Giemsa staining, however, suffered from limited resolution. In particular, the human genome could only be divided into as many as 350 to 850 bands by conventional Giemsa staining

techniques. The effective resolution of genetic maps based on such techniques was limited to about 5 to 10 megabases.

Hybridization techniques such as fluorescence in situ hybridization revolutionized genetic mapping techniques. With such hybridization techniques the resolution of genetic mapping techniques can be improved to resolutions of about 50 kilobases to 100 kilobases or even greater. However, such mapping techniques based on hybridization require specific hybridization probes in order to be effective. Polynucleotides comprising SEQ ID NOS:9-18 provide additional specific probes that can be used to improve the utility of current genetic mapping techniques. Since the use of a polynucleotide comprising one of SEQ ID NOS:9-18 for mapping specifically identifies the genomic location corresponding to the polynucleotide, the use is specific for the polynucleotide.

Since polynucleotides comprising SEQ ID NOS:9-18 can be used to expand the utility of genomic data, to expand the utility of current mapping techniques and for the other utilities discussed above and in the specification, Applicants submit such polynucleotides satisfy the requirements for patentability under 35 U.S.C. § 101. Applicants therefore respectfully request that the rejection of Claim 3 under 35 U.S.C. § 101 be withdrawn. Applicants also submit that new Claims 10-14 meet the requirements for patentability under 35 U.S.C. § 101.

#### **VI. REJECTION UNDER 35 U.S.C. § 112, FIRST PARAGRAPH (UTILITY)**

Claims 1-4 stand rejected under 35 U.S.C. § 112, first paragraph, as allegedly lacking utility. Applicants note that Claims 1, 2 and 4 have been canceled without prejudice with the present Amendment. Applicants traverse this rejection on the ground that Claim 3 has significant patentable utility as discussed in Section V, above. Applicants respectfully request that the rejection of Claim 3 under 35 U.S.C. § 112, first paragraph, be withdrawn. Applicants also submit that new Claims 10-14 meet the requirements for patentability under 35 U.S.C. § 112, first paragraph.

#### **VII. REJECTION UNDER 35 U.S.C. § 112, FIRST PARAGRAPH, (WRITTEN DESCRIPTION)**

Claims 1-4 stand rejected under 35 U.S.C. § 112, first paragraph, as allegedly containing subject matter that was not described in the specification. Applicants note that Claims 1, 2 and 4 have been canceled without prejudice with the present Amendment.

Applicants traverse this rejection on the ground that amended Claim 3 is fully supported by the specification and claims as originally filed.

35 U.S.C. § 112, first paragraph, requires that the specification contain a written description of the invention. An applicant must convey with reasonably clarity to those skilled in the art that the applicant was in possession of the invention. *Vas-Cath v. Mahurkar*, 19 USPQ2d 1111, 1117 (Fed. Cir. 1991). An adequate description of a chemical genus requires a precise definition by *structure, formula, chemical name or physical properties* sufficient to distinguish the genus from other materials. *Fiers v. Revel*, 25 USPQ2d 1601, 1606 (Fed. Cir. 1993). The standard for claims involving chemical materials has been explicitly stated by the Federal Circuit:

In claims involving chemical materials, generic formulae usually indicate with specificity what the generic claims encompass. One skilled in the art can distinguish such a formula from others and can identify many of the species that the claims encompass. Accordingly, such a formula is normally an adequate description of the claimed genus. *Univ. of California v. Eli Lilly and Co.*, 43 USPQ2d 1398, 1406 (Fed. Cir. 1997).

However, description of the function of genetic material is not an adequate description of the genetic material:

In claims to genetic material...a generic statement such as “vertebrate insulin cDNA” or “mammalian insulin cDNA,” without more, is not an adequate written description of the genus because it does not distinguish the claimed genus from others, except by function. It does not specifically define any of the genes that fall within its definition. It does not define any structural features commonly possessed by members of the genus that distinguish them from others. One skilled in the art cannot, as one can do with a fully described genus, visualize or recognize the identity of the members of the genus. *Id.*

Thus, a claim describing a genus of nucleic acid by *structure, formula, chemical name or physical properties* sufficient to distinguish the genus from other materials meets the written description requirement of 35 U.S.C. § 112, first paragraph, as elaborated by the Federal Circuit in *Fiers v. Revel* and in *Univ. of California v. Eli Lilly and Co.*

Claims 3 and 10-14 recite isolated polynucleotides corresponding to at least one of SEQ ID NOS:9-18. The isolated polynucleotides are fully described by *structure* or by *physical properties*, or both, sufficient to distinguish the claimed isolated polynucleotides from other materials.

For instance, Claim 3 recites an isolated polynucleotide that comprises a contiguous stretch of at least about 60 nucleotides of at least one of SEQ ID NOS:10-12, 15, 16. Given the description of Claim 3, one of skill in the art can readily distinguish the isolated polynucleotides of Claim 3 from other materials by the *structural* description of Claim 3. If an isolated polynucleotide comprises a contiguous stretch of at least about 60 nucleotides of at least one of SEQ ID NOS:10-12, 15, 16, the isolated polynucleotide is within the genus of Claim 3. Other chemical materials that lack this *structural* feature are not within the genus. Claims 10-13 similarly recite genera of isolated polynucleotides with precise *structural* definitions of chemical genera.

New Claim 14 recites an isolated polynucleotide capable of hybridizing to a polynucleotide of Claim 3 or 10. New Claim 14 describes a genus of polynucleotides by a *physical property* that readily distinguishes the claimed polynucleotides from other materials. In particular, those polynucleotides with the *physical property* of being capable of hybridizing to a polynucleotide of Claim 3 or 10 are within the genus of Claim 14. Other chemical materials that lack this *physical property* are not within the genus. One of skill in the art can readily distinguish the polynucleotides of Claim 14 from other materials. New Claim 14 thus meets the written description requirement.

Since Claim 3 meets the written description requirement, Applicants respectfully request that the rejection of Claims 3 under 35 U.S.C. § 112, first paragraph, be withdrawn. Applicants also submit that new Claims 10-14 meet the requirements for patentability under 35 U.S.C. § 112.

#### **VIII. THE REJECTIONS UNDER 35 U.S.C. § 102(b)**

Claims 1-3 stand rejected under 35 U.S.C. § 102(a) or (b) as allegedly being anticipated by at least one of several references. Claim 1 and 2 stand rejected as allegedly being anticipated by Miao & Verma, 1993, Accession No. SOYNOD26A; by Matsubara & Okubo, 1996, Accession No. T21573; by Waterson, 1998, Accession No. AC004977; by Lee *et al.*, 1998, Accession No. H33155; or by NCI-CGAP, 1997, Accession No. AA650451. Claims 1-3 stand rejected as allegedly being anticipated by Martin *et al.*, 1995, Accession No. HUM22DC98Z; by Hillier *et al.*, 1996, Accession No. AA157818; by NCI-CGAP, 1998, Accession No. AI076014; or by NCI-CGAP, 1997, Accession No. AA493099. Since Claims 1 and 2 have been canceled without prejudice, Applicants submit that the rejections of

Claims 1 and 2 are moot. Applicants traverse the rejections of Claim 3 on the ground that none of the references cited by the PTO teach or suggest each and every element of amended Claim 3.

The standard for anticipation under 35 U.S.C. §102 is strict identity. Anticipation under § 102 can only be established by a single prior art reference that teaches each and every element of the claimed invention. *Structural Rubber Products Co. v. Park Rubber Co.* 223 USPQ 1264 (1984).

Amended Claim 3 recites an isolated polynucleotide comprising a contiguous stretch of at least about 60 nucleotides of at least one of SEQ ID NOS:10-12, 15, 16. Claim 10 recites an isolated polynucleotide that comprises a contiguous stretch of at least about 30 nucleotides of SEQ ID NO:10, 11, 15, 16. Claim 11 recites an isolated polynucleotide that comprises a contiguous stretch of at least about 100 nucleotides of at least one of SEQ ID NO:9-17. Claim 12 recites an isolated polynucleotide that comprises a contiguous stretch of at least about 130 nucleotides of at least one of SEQ ID NO:9-18. Claim 13 recites an isolated polynucleotide that comprises at least one of SEQ ID NOS:9-18. Claim 14 recites an isolated polynucleotide is capable of hybridizing to a polynucleotide of Claim 3, 10 or 11.

Accession No. HUM22DC98Z does not teach or suggest each and every element of amended Claim 3 or new Claims 10-14. The PTO asserts that Accession No. HUM22DC98Z teaches an oligonucleotide comprising a contiguous stretch of 75 bases of SEQ ID NO:9. However, Accession No. HUM22DC98Z does not teach or suggest an isolated polynucleotide comprising a contiguous stretch of at least about 100 or 130 nucleotides of SEQ ID NO:9. As such, Accession No. HUM22DC98Z does not teach or suggest each and every element of Claims 3 or 10-14.

Accession No. SOYNOD26A does not teach or suggest each and every element of amended Claim 3 or new Claims 10-14. The PTO asserts that Accession No. SOYNOD26A teaches an oligonucleotide comprising a contiguous stretch of 21 bases of SEQ ID NO:10. However, Accession No. SOYNOD26A does not teach or suggest an isolated polynucleotide comprising a contiguous stretch of at least about 30, 60, 100 or 130 nucleotides of SEQ ID NO:10. As such, Accession No. SOYNOD26A does not teach or suggest each and every element of Claims 3 or 10-14.

Accession No. T21573 does not teach or suggest each and every element of amended Claim 3 or new Claims 10-14. The PTO asserts that Accession No. T21573 teaches an

oligonucleotide comprising a contiguous stretch of 21 bases of SEQ ID NO:11. However, Accession No. T21573 does not teach or suggest an isolated polynucleotide comprising a contiguous stretch of at least about 30, 60, 100 or 130 nucleotides of SEQ ID NO:11. As such, Accession No. T21573 does not teach or suggest each and every element of Claims 3 or 10-14.

Accession No. AC004977 does not teach or suggest each and every element of amended Claim 3 or new Claims 10-14. The PTO asserts that Accession No. AC004977 teaches an oligonucleotide comprising a contiguous stretch of 45 bases of SEQ ID NO:12. However, Accession No. AC004977 does not teach or suggest an isolated polynucleotide comprising a contiguous stretch of at least about 60, 100 or 130 nucleotides of SEQ ID NO:12. As such, Accession No. AC004977 does not teach or suggest each and every element of Claims 3 or 10-14.

Accession No. AA157818 does not teach or suggest each and every element of amended Claim 3 or new Claims 10-14. The PTO asserts that Accession No. AA157818 teaches an oligonucleotide comprising a contiguous stretch of 74 bases of SEQ ID NO:13. However, Accession No. AA157818 does not teach or suggest an isolated polynucleotide comprising a contiguous stretch of at least about 100 or 130 nucleotides of SEQ ID NO:13. As such, Accession No. AA157818 does not teach or suggest each and every element of Claims 3 or 10-14.

Accession No. AI076014 does not teach or suggest each and every element of amended Claim 3 or new Claims 10-14. The PTO asserts that Accession No. AI076014 teaches an oligonucleotide comprising a contiguous stretch of 82 bases of SEQ ID NO:14. However, Accession No. AI076014 does not teach or suggest an isolated polynucleotide comprising a contiguous stretch of at least about 100 or 130 nucleotides of SEQ ID NO:14. As such, Accession No. AI076014 does not teach or suggest each and every element of Claims 3 or 10-14.

Accession No. H33155 does not teach or suggest each and every element of amended Claim 3 or new Claims 10-14. The PTO asserts that Accession No. H33155 teaches an oligonucleotide comprising a contiguous stretch of 21 bases of SEQ ID NO:15. However, Accession No. H33155 does not teach or suggest an isolated polynucleotide comprising a contiguous stretch of at least about 30, 60, 100 or 130 nucleotides of SEQ ID NO:15. As

such, Accession No. H33155 does not teach or suggest each and every element of Claims 3 or 10-14.

Accession No. AA650451 does not teach or suggest each and every element of amended Claim 3 or new Claims 10-14. The PTO asserts that Accession No. AA650451 teaches an oligonucleotide comprising a contiguous stretch of 19 bases of SEQ ID NO:16. However, Accession No. AA650451 does not teach or suggest an isolated polynucleotide comprising a contiguous stretch of at least about 30, 60, 100 or 130 nucleotides of SEQ ID NO:16. As such, Accession No. AA650451 does not teach or suggest each and every element of Claims 3 or 10-14.

Accession No. AA493099 does not teach or suggest each and every element of amended Claim 3 or new Claims 10-14. The PTO asserts that Accession No. AA493099 teaches an oligonucleotide comprising a contiguous stretch of 72 bases of SEQ ID NO:17 and an oligonucleotide comprising a contiguous stretch of 119 bases of SEQ ID NO:18. However, Accession No. AA493099 does not teach or suggest an isolated polynucleotide comprising a contiguous stretch of at least about 100 or 130 nucleotides of SEQ ID NO:17. Furthermore, Accession No. AA493099 does not teach or suggest an isolated polynucleotide comprising a contiguous stretch of at least about 130 nucleotides of SEQ ID NO:18. As such, Accession No. AA493099 does not teach or suggest each and every element of Claims 3 or 10-14.

Since Accession Nos. HUM22DC98Z, SOYNOD26A, T21573, AC004977, AA157818, AI076014, H33155, AA650451 and AA493099, alone or in any combination, do not teach or suggest each and every element of amended Claim 3, these references do not anticipate Claim 3. Applicants request that the rejections of Claim 3 under 35 U.S.C. § 102 be withdrawn. In addition, Applicants submit that new Claims 10-14 meet the requirements for patentability under 35 U.S.C. § 102.

### **CONCLUSION**

Applicants submit that Claims 3 and 10-14 satisfy all of the criteria for patentability and are in condition for allowance. An early indication of the same and passage of Claims 3 and 10-14 to issuance is therefore kindly solicited.

No fees in addition to the extension fee are believed due in connection with this response. However, the Commissioner is authorized to charge all required fees, fees under 37

C.F.R. § 1.17 and all required extension of time fees, or credit any overpayment, to Pennie & Edmonds U.S. Deposit Account No. 16-1150.

Respectfully submitted,

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